

SEQUENCE LISTING

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<120> Gamma-Conopeptides

<130> 2314-147-sq2

<140>  
<141>

<150> US 60/069,706  
<151> 1997-12-16

<160> 47

<170> PatentIn Ver. 2.0

<210> 1  
<211> 42  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:generic formula  
of gamma-conopeptides

<220>  
<221> PEPTIDE  
<222> (1)..(13)  
<223> Xaa at residues 1, 2, 3, 4, 5, and 6 may be  
des-Xaa or any amino acid; Xaa at residues 8, 9,  
10, 11 and 12 may be any amino acid; Xaa at  
residue 13 may be des-Xaa or any amino acid.

<220>  
<221> PEPTIDE  
<222> (15)..(19)  
<223> Xaa at residues 15, 16, 17 and 18 may be any amino  
acid; Xaa at residue 19 is Glu,  
gamma-carboxyglutamate or Gln.

<220>  
<221> PEPTIDE  
<222> (22)..(28)  
<223> Xaa at residues 22, 23 and 24 may be any amino  
acid; Xaa at residue 25 may be des-Xaa or any  
amino acid; Xaa at residues 27, 28 and 29 may be  
any amino acid.

<220>  
<221> PEPTIDE

<222> (30)..(42)  
<223> Xaa at residues 30, 31 and 32 may be des-Xaa or  
any amino acid; Xaa at residues 34, 35, 36, 37,  
38, 39, 40, 41 and 42 may be des-Xaa or any amino  
acid.

<400> 1  
Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15  
Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30  
Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40

<210> 2  
<211> 42  
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<220>  
<223> Description of Artificial Sequence:generic  
sequence of gamma-conopeptides.

<220>  
<221> PEPTIDE  
<222> (1)..(13)  
<223> Xaa at residues 1, 2, 3, 4, 5 and 6 may be des-Xaa  
or any amino acid; Xaa at residues 8, 9, 10, 11  
and 12 may be any amino acid; Xaa at residue 13  
may be des-Xaa or any amino acid.

<220>  
<221> PEPTIDE  
<222> (15)..(22)  
<223> Xaa at residues 15, 16, 17 and 18 may be any amino  
acid; Xaa at residue 19 is Glu,  
gamma-carboxyglutamate or Gln; Xaa at residue 22  
is Ser or Thr.

<220>  
<221> PEPTIDE  
<222> (23)..(29)  
<223> Xaa at residues 23 and 24 may be any amino acid;  
Xaa at residue 25 may be des-Xaa or any amino  
acid; Xaa at residues 27, 28 and 29 may be any  
amino acid.

<220>  
<221> PEPTIDE  
<222> (30)..(42)  
<223> Xaa at residues 30, 31 and 32 may be des-Xaa or  
any amino acid; Xaa at residues 34, 35, 36, 37,  
38, 39, 40, 41 and 42 may be des-Xaa or any amino  
acid.

<400> 2  
Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15  
Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 35 40

<210> 3  
 <211> 39  
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 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:generic formula  
 of gamma-conopeptides

<220>  
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 <222> (1)..(13)  
 <223> Xaa at residue 1 is any amino acid; Xaa at  
 residues 2, 3, 4, 5 and 6 may be des-Xaa or any  
 amino acid; Xaa at residues 8, 9, 10, 11, 12 and  
 13 may be any amino acid.

<220>  
 <221> PEPTIDE  
 <222> (27)..(39)  
 <223> Xaa at residues 27, 28, 29, 31, 32, 33, 34, 35, 36  
 and 37 may be any amino acid; Xaa at residues 38  
 and 39 may be des-Xaa or any amino acid.

<220>  
 <221> PEPTIDE  
 <222> (15)..(19)  
 <223> Xaa at residues 15, 16, 17 and 18 may be any amino  
 acid; Xaa at residue 19 is Glu or  
 gamma-carboxyglutamate.

<400> 3  
 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
 1 5 10 15  
 Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Xaa Xaa Cys Xaa Xaa  
 20 25 30  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 35

<210> 4  
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<220>  
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 sequence of gamma-conopeptides.

<220>  
 <221> PEPTIDE  
 <222> (1)..(13)  
 <223> Xaa at residue 1 is any amino acid; Xaa at  
 residues 2, 3, 4, 5 and 6 may be des-Xaa or any  
 amino acid; Xaa at residues 8, 9, 10, 11, 12 and  
 13 may be any amino acid.

<220>

<221> PEPTIDE  
 <222> (15)..(19)  
 <223> Xaa at residue 15 is Ser or Thr; Xaa at residues  
 16, 17 and 18 may be any amino acid; Xaa at  
 residue 19 is Glu or gamma-carboxyglutamate.

<220>  
 <221> PEPTIDE  
 <222> (27)..(39)  
 <223> Xaa at residues 27, 28, 29, 31, 32, 33, 34, 35, 36  
 and 37 may be any amino acid; Xaa at residues 38  
 and 39 may be des-Xaa or any amino acid.

<400> 4  
 Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
 1 5 10 15

Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Xaa Xaa Cys Xaa Xaa  
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 35

<210> 5  
 <211> 34  
 <212> PRT  
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<220>  
 <223> Description of Artificial Sequence:generic  
 sequence of gamma-conopeptides.

<220>  
 <221> PEPTIDE  
 <222> (1)..(6)  
 <223> Xaa at residues 1 and 2 may be des-Xaa or any  
 amino acid; Xaa at residue 3 is Asp, Glu or  
 gamma-carboxyglutamate; Xaa at residues 5 and 6  
 may be any amino acid.

<220>  
 <221> PEPTIDE  
 <222> (7)..(16)  
 <223> Xaa at residue 7 is Trp or 6-bromo-Trp; Xaa at  
 residues 9, 10, 13 and 14 may be any amino acid;  
 Xaa at residue 16 is Glu or  
 gamma-carboxyglutamate.

<220>  
 <221> PEPTIDE  
 <222> (28)..(34)  
 <223> Xaa at residues 28, 30, 31, 32, 33 and 34 may be  
 any amino acid.

<400> 5  
 Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Cys Thr Xaa Xaa Ser Xaa  
 1 5 10 15

Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Xaa Xaa Xaa  
 20 25 30

Xaa Xaa

<210> 6  
 <211> 32  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at residues 14 and 26 are Glu or gamma-carboxyglutamate; Xaa at residue 31 is Pro or hydroxy-Pro.

<400> 6  
 Asp Cys Thr Ser Xaa Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys  
 1 5 10 15  
 Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser  
 20 25 30

<210> 7  
 <211> 34  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(34)  
 <223> Xaa at residues 1, 7 and 34 are Trp or 6-bromo-Trp; Xaa at residues 3 and 16 are Glu or gamma-carboxyglutamate; Xaa at residues 31 and 32 are Pro or hydroxy-Pro.

<400> 7  
 Xaa Leu Xaa Cys Ser Val Xaa Phe Ser His Cys Thr Lys Asp Ser Xaa  
 1 5 10 15  
 Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Xaa Xaa  
 20 25 30

Asp Xaa

<210> 8  
 <211> 39  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(39)  
 <223> Xaa at residues 1, 2, 4, 10 and 39 are Trp or 6-bromo-Trp ; Xaa at residues 19 and 31 are Glu or gamma-carboxyglutamate; Xaa at residues 34, 36 and 37 are Pro or hydroxy-Pro.

<400> 8  
 Xaa Xaa Arg Xaa Gly Gly Cys Met Ala Xaa Phe Gly Leu Cys Ser Arg

Met Xaa Phe Xaa Xaa Asp Xaa  
35

<400> 9  
Cys Lys Thr Tyr Ser Lys Tyr Cys Xaa Ala Asp Ser Xaa Cys Cys Thr  
1 5 10 15

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<210> 10
<211> 34
<212> PRT
<213> Conus textile
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<400> 10
Asp Xaa Xaa Asp Asp Gly Cys Ser Val Xaa Gly Xaa Cys Thr Tyr Asn
 1          5          10          15
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Xaa Val

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<210> 11
<211> 31
<212> PRT
<213> Conus textile
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<220>
<221> PEPTIDE
<222> (1)..(31)
<223> Xaa at residues 3 and 31 are Trp of 6-bromo-Trp;
Xaa at residues 5, 18, 22 and 25 are Glu or
gamma-carboxyglutamate; Xaa at residue 16 is Pro
or hydroxy-Pro.

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<400> 11  
 Gly Met Xaa Gly Xaa Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Xaa  
           1                  5                  10                  15  
 Ser Xaa Cys Cys Ser Xaa Asp Cys Xaa Gly Ser Cys Thr Met Xaa  
                   20                  25                  30

<210> 12  
 <211> 32  
 <212> PRT  
 <213> Conus gloriamaris

<220>  
 <221> PEPTIDE  
 <222> (1)..(32)  
 <223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at  
 residue 1 is Glu or gamma-carboxyglutamate; Xaa at  
 residues 8 and 11 are Pro or hydroxy-Pro.

<400> 12  
 Xaa Cys Arg Ala Xaa Tyr Ala Xaa Cys Ser Xaa Gly Ala Gln Cys Cys  
           1                  5                  10                  15  
 Ser Leu Leu Met Cys Ser Lys Ala Thr Ser Arg Cys Ile Leu Ala Leu  
                   20                  25                  30

<210> 13  
 <211> 29  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(29)  
 <223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp;  
 Xaa at residues 5, 16 and 23 are Glu or  
 gamma-carboxyglutamate; Xaa at residue 10 is Pro  
 or hydroxy-Pro.

<400> 13  
 Asn Gly Gln Cys Xaa Asp Val Xaa Met Xaa Cys Thr Ser Asn Xaa Xaa  
           1                  5                  10                  15  
 Cys Cys Ser Leu Asp Cys Xaa Met Tyr Cys Thr Gln Ile  
                   20                  25

<210> 14  
 <211> 27  
 <212> PRT  
 <213> Conus marmoreus

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residue 4 is Trp or 6-bromo-Trp; Xaa at  
 residues 9, 12, 13 and 17 are Glu or  
 gamma-carboxyglutamate.

<400> 14  
Cys Gly Gly Xaa Ser Thr Tyr Cys Xaa Val Asp Xaa Xaa Cys Cys Ser  
1 5 10 15

Xaa Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe  
20 25

<210> 15  
<211> 26  
<212> PRT  
<213> Conus marmoreus

<220>  
<221> PEPTIDE  
<222> (1)..(26)  
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp;  
Xaa at residue 16 is Glu or  
gamma-carboxyglutamate.

<400> 15  
Asn Gly Gly Cys Lys Ala Thr Xaa Met Ser Cys Ser Ser Gly Xaa Xaa  
1 5 10 15

Cys Cys Ser Met Ser Cys Asp Met Tyr Cys  
20 25

<210> 16  
<211> 323  
<212> DNA  
<213> Conus textile

<220>  
<221> CDS  
<222> (1)..(153)

<400> 16  
gaa cgg gct aag atc aac ttg ctt cca aag aga aag cca cct gct gag 48  
Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu  
1 5 10 15  
cgt tgg ttg gaa tgc agt gtt tgg ttt tca cat tgt acg aag gac tcg 96  
Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser  
20 25 30  
gaa tgt tgt tct aat agt tgt gac caa acg tac tgc acg tta atg cca 144  
Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro  
35 40 45  
ccg gac tgg tgacatcgcc actctcctgt tcagagtctt caaggctttt 193  
Pro Asp Trp  
50  
gttctctttt gaagaatttt aacgagtga caaaaaagtg gactagcatg tttccttttc 253  
cctttgcaaa atcaatgatg gaggtaaaag cctcccattt tgtcttcatc aataaagaac 313  
ttatcatcat 323

<210> 17  
<211> 51  
<212> PRT



<213> Conus textile

<400> 17

Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu  
1 5 10 15

Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser  
20 25 30

Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro  
35 40 45

Pro Asp Trp  
50

<210> 18

<211> 510

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (95)..(337)

<400> 18

tgactcgcca tctcctctct cagtctccct gacagctgcc ttcagtcgac cctgccgtca 60

tctcaacgca cacttgaagt gaaaaacctt tatc atg gag aaa ctg aca att ctg 115  
Met Glu Lys Leu Thr Ile Leu  
1 5

ctt ctt gtt gct gct gta ctg ttg tgc atc cag gcc cta aat caa gaa 163  
Leu Leu Val Ala Ala Val Leu Leu Ser Ile Gln Ala Leu Asn Gln Glu  
10 15 20

aaa cac caa cgg gca aag atc aac ttg ctt tca aag aga aag cca cct 211  
Lys His Gln Arg Ala Lys Ile Asn Leu Leu Ser Lys Arg Lys Pro Pro  
25 30 35

gct gag cgt tgg tgg cgg tgg gga gga tgc atg gct tgg ttt ggg ctt 259  
Ala Glu Arg Trp Trp Arg Trp Gly Gly Cys Met Ala Trp Phe Gly Leu  
40 45 50 55

tgt tgc agg gac tgc gaa tgt tgt tct aat agt tgt gac gta acg cgc 307  
Cys Ser Arg Asp Ser Glu Cys Cys Ser Asn Ser Cys Asp Val Thr Arg  
60 65 70

tgc gag tta atg cca ttc cca cca gac tgg tgacatcgac actctcctct 357  
Cys Glu Leu Met Pro Phe Pro Pro Asp Trp  
75 80

tcagagtctt caaggctttt gttctctttt gaagaatttt tacgagttaa caaaaacgtg 417

gactagcacg tttccttttc cctttgcaaa atcaatgatg gaggtaaaag tgtcccattt 477

tgtcttcacg aataaagaac ttatcatcat aat 510

<210> 19

<211> 81

<212> PRT

<213> Conus textile

<400> 19

Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser  
1 5 10 15

Ile Gln Ala Leu Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn Leu  
20 25 30

Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly Gly  
35 40 45

Cys Met Ala Trp Phe Gly Leu Cys Ser Arg Asp Ser Glu Cys Cys Ser  
50 55 60

Asn Ser Cys Asp Val Thr Arg Cys Glu Leu Met Pro Phe Pro Pro Asp  
65 70 75 80

Trp

<210> 20

<211> 441

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (16)..(243)

<400> 20

ggaâââactt ttatc atg gag aaa ctg aca atc ctg ctc ctt gtt gct gct 51  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala  
1 5 10

gta ctg atg tgc acc cag gcc atg ttt caa ggt gat gga gaa aaa tcc 99  
Val Leu Met Ser Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser  
15 20 25

cgg aag gcg gag atc aac ttt tct gaa aca aga aag ttg gcg aga aac 147  
Arg Lys Ala Glu Ile Asn Phe Ser Glu Thr Arg Lys Leu Ala Arg Asn  
30 35 40

aag cag aaa cgc tgc aaa act tat tca aag tat tgt gaa gct gac tgc 195  
Lys Gln Lys Arg Cys Lys Thr Tyr Ser Lys Tyr Cys Glu Ala Asp Ser  
45 50 55 60

gaa tgc tgt acc gaa cag tgt gta agg tct tac tgc acg ttg ttt gga 243  
Glu Cys Cys Thr Glu Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
65 70 75

tgaattcgga ccacaagcca tcgatataca cccctctcct cttcagaggc ttcaaggctt 303

ttgtttatcct tttgaagaat ctttatcgag taaacataag tagacaagct ttttttttcc 363

tttgcaaaat gaagaatgat ggcaaaaagc cccccatttt gtcttcatca ataaagaact 423

cgctatcaga ataaaaaa 441

<210> 21

<211> 76

<212> PRT

<213> Conus textile

<400> 21

Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
 1 5 10 15  
 Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser Arg Lys Ala Glu  
 20 25 30  
 Ile Asn Phe Ser Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Lys Arg  
 35 40 45  
 Cys Lys Thr Tyr Ser Lys Tyr Cys Glu Ala Asp Ser Glu Cys Cys Thr  
 50 55 60  
 Glu Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
 65 70 75

<210> 22

<211> 460

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (49)..(273)

<400> 22

ctgccgtcat ctcagcgcac acttggttaag aagtgaaaaa ccttgatc atg gag aaa 57  
 Met Glu Lys  
 1  
 ctg aca att ctg ctt ctt gtt gct gct gtg ctg atg tcg acc cag gcc 105  
 Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
 5 10 15  
 cta att caa gat caa cgc caa aag gca aag atc aac ttg ttt tca aag 153  
 Leu Ile Gln Asp Gln Arg Gln Lys Ala Lys Ile Asn Leu Phe Ser Lys  
 20 25 30 35  
 aga cag gca tat gct cgt gat tgg tgg gac gat ggc tgc agt gtg tgg 201  
 Arg Gln Ala Tyr Ala Arg Asp Trp Trp Asp Asp Gly Cys Ser Val Trp  
 40 45 50  
 ggg cct tgt acg gtg aac gca gaa tgt tgt tct ggt gat tgt cat gaa 249  
 Gly Pro Cys Thr Val Asn Ala Glu Cys Cys Ser Gly Asp Cys His Glu  
 55 60 65  
 acg tgc att ttc ggg tgg gaa gtc tgaccacaaa ccatccgaca tcgccactct 303  
 Thr Cys Ile Phe Gly Trp Glu Val  
 70 75  
 cctcttcaga gacttcaagg cttttgttct cttttgaaga attttacgag tgagcaaaaa 363  
 ggtagactag cacgtttctt tttccctttg caaatcaat gatggaggta aaagcctccc 423  
 attttgtct catcaataaa gaacttatca tcataat 460

<210> 23

<211> 75

<212> PRT

<213> Conus textile

<400> 23

Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
 1 5 10 15  
 Thr Gln Ala Leu Ile Gln Asp Gln Arg Gln Lys Ala Lys Ile Asn Leu  
 20 25 30  
 Phe Ser Lys Arg Gln Ala Tyr Ala Arg Asp Trp Trp Asp Asp Gly Cys  
 35 40 45  
 Ser Val Trp Gly Pro Cys Thr Val Asn Ala Glu Cys Cys Ser Gly Asp  
 50 55 60  
 Cys His Glu Thr Cys Ile Phe Gly Trp Glu Val  
 65 70 75

<210> 24  
 <211> 533  
 <212> DNA  
 <213> Conus textile

<220>  
 <221> CDS  
 <222> (110)..(337)

<400> 24  
 ctctgccggt tgacacntca tctactctct cagtctccct gacagctgcc ttcagtcgac 60  
 cctgccgtca tctcagcgca gacttgataa gaagtgaata acctttatc atg gag aaa 118  
 Met Glu Lys  
 1  
 ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag gcc 166  
 Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
 5 10 15  
 ctg gtt gaa cgt gct gga gaa aac cac tca aag gag aac atc aat ttt 214  
 Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn Ile Asn Phe  
 20 25 30 35  
 tta tta aaa aga aag aga gct gct gac agg ggg atg tgg ggc gaa tgc 262  
 Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp Gly Glu Cys  
 40 45 50  
 aaa gat ggg tta acg aca tgt ttg gcg ccc tca gag tgt tgt tct gag 310  
 Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys Cys Ser Glu  
 55 60 65  
 gat tgt gaa ggg agc tgc acg atg tgg tgatgaattc tgaccacaag 357  
 Asp Cys Glu Gly Ser Cys Thr Met Trp  
 70 75  
 ccatctgaca tcaccactct cctcttcaga ggcttcaagg cttttgtttt ccttttgaat 417  
 aatctttacg agtaaacaaa taagtagact agcgcgtttt tttccctttg agaaatcaat 477  
 gatggaggta aatagcttcc tattttgtct tattcaataa agaacttatc ataata 533

<210> 25  
 <211> 76  
 <212> PRT  
 <213> Conus textile

<400> 25

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Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser
 1           5           10           15
Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn
          20           25           30
Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp
          35           40           45
Gly Glu Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys
          50           55           60
Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp
          65           70           75

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<210> 26

<211> 408

<212> DNA

<213> Conus gloriamaris

<220>

<221> CDS

<222> (2)..(211)

<400> 26

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g ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag gcc 49
  Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
   1           5           10           15
ctg att caa ggt ggt ggt gac aaa cgt caa aag gca aac atc aac ttt 97
  Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe
           20           25           30
ctt tca agg tgg gac cgt gag tgc agg gct tgg tat gcg ccg tgt agc 145
  Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser
           35           40           45
cct ggc gcg caa tgt tgt agt ttg ctg atg tgt tca aaa gcg acc agc 193
  Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser
           50           55           60
cgc tgc ata ttg gcg tta tgaactctga ccacaagcca tccgacatca 241
  Arg Cys Ile Leu Ala Leu
   65           70
ccactctcct cttcagaggc ttcaaggctt tttgtttttc ttttgaagaa tctttacgag 301
tgaacaaaata agtagaatag cacgtttttc cccctttgca aaatcaataa tggagggttaa 361
aaaaaaaaactt ctgtcttctt caataaagaa gttatcataa taaaaaa 408

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<210> 27

<211> 70

<212> PRT

<213> Conus gloriamaris

<400> 27

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Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala
 1           5           10           15
Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe

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	20		25		30										
Leu	Ser	Arg	Trp	Asp	Arg	Glu	Cys	Arg	Ala	Trp	Tyr	Ala	Pro	Cys	Ser
	35					40						45			
Pro	Gly	Ala	Gln	Cys	Cys	Ser	Leu	Leu	Met	Cys	Ser	Lys	Ala	Thr	Ser
	50					55						60			
Arg	Cys	Ile	Leu	Ala	Leu										
65					70										

<210> 28  
 <211> 278  
 <212> DNA  
 <213> Conus marmoreus

<220>  
 <221> CDS  
 <222> (4)..(222)

<400> 28  
 atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gtg ctg ctg 48  
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu  
 1 5 10 15  
 tcg acc cag gcc cta aat caa gaa aaa cgc cca aag gag atg atc aat 96  
 Ser Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn  
 20 25 30  
 ttt tta tca aaa gga aag aca aat gct gag agg cgg aac ggc caa tgc 144  
 Phe Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys  
 35 40 45  
 gag gat gtt tgg atg cct tgt aca tcg aac tgg gaa tgc tgt tct ttg 192  
 Glu Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu  
 50 55 60  
 gat tgt gaa atg tac tgc aca cag ata gga tgaactctga ccacaagcca 242  
 Asp Cys Glu Met Tyr Cys Thr Gln Ile Gly  
 65 70  
 tccgacatca ccactctcct cttcagagtc ttcaag 278

<210> 29  
 <211> 73  
 <212> PRT  
 <213> Conus marmoreus

<400> 29  
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser  
 1 5 10 15  
 Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn Phe  
 20 25 30  
 Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys Glu  
 35 40 45  
 Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu Asp  
 50 55 60  
 Cys Glu Met Tyr Cys Thr Gln Ile Gly

65

70

<210> 30  
<211> 287  
<212> DNA  
<213> Conus marmoreus

<220>  
<221> CDS  
<222> (4)..(231)

<400> 30  
atc atg gag aaa ctg aca atc ctg ctt ctt gtt gct gct gta ctg ata 48  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile 15  
1 5 10  
ccg acc cag gcc ctt ttt caa ggt gat gac gga aaa tcc cag aag gcg 96  
Pro Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala 30  
20 25  
gag atc aag tct ttt gaa aca aga aag tta gcg aga aac aag cag gta 144  
Glu Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val 45  
35 40  
cgc tgc ggt ggt tgg tca acg tat tgt gaa gtt gac gag gaa tgc tgt 192  
Arg Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys 60  
50 55  
tcg gaa tca tgt gta agg tct tac tgc acg ctg ttt gga tgaactcgga 241  
Ser Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly 75  
65 70  
ccacaagcca tccgatatca ccactctcct gtccagagtc ttcaag 287

<210> 31  
<211> 76  
<212> PRT  
<213> Conus marmoreus

<400> 31  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile Pro 15  
1 5 10  
Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala Glu 30  
20 25  
Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val Arg 45  
35 40  
Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys Ser 60  
50 55  
Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly 75  
65 70

<210> 32  
<211> 278  
<212> DNA  
<213> Conus marmoreus

<220>

<221> CDS

<222> (4)..(213)

<400> 32

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atc atg cag aaa ctg ata att ctg ctt ctt gtt gct gct gtg ctg atg 48
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met
1 5 10 15

acg acc cag gcc cta tat caa gaa aaa cgc cga aag gag atg atc aat 96
Thr Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn
20 25 30

ttt tta tca aaa gga aag ata aat gct gag agg cgg aac ggc gga tgc 144
Phe Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys
35 40 45

aaa gct act tgg atg tct tgt tca tgc ggc tgg gaa tgc tgt tct atg 192
Lys Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met
50 55 60

agt tgt gac atg tac tgc gga tagataggat gaactctgac cacaagccat 243
Ser Cys Asp Met Tyr Cys Gly
65 70

ccgacatcac cactctcctc ttcagagtct tcaag 278

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<210> 33

<211> 70

<212> PRT

<213> Conus marmoreus

<400> 33

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Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Thr
1 5 10 15

Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn Phe
20 25 30

Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys Lys
35 40 45

Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met Ser
50 55 60

Cys Asp Met Tyr Cys Gly
65 70

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<210> 34

<211> 528

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (98)..(316)

<400> 34

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gcacgtcatc ttctctctca gtctgctga cagctgcctt cagtcaaccc tgccgtcatc 60

tcacgcgtaga cttggtaaga agtgaaaaac atttata atg cag aaa ctg ata atc 115
Met Gln Lys Leu Ile Ile
1 5

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<400> 36  
Leu Cys Xaa Asp Tyr Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys  
1 5 10 15

Ser Xaa Asn Cys Tyr Asn Gly His Cys Thr  
20 25

<210> 37  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
gamma-conopeptide sequence for probe

<220>  
<221> PEPTIDE  
<222> (1)  
<223> Xaa is Glu or Gln.

<400> 37  
Xaa Cys Cys Ser  
1

<210> 38  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:degenerate  
probe for consensus gamma-conopeptide sequence.

<400> 38  
sartgytggya gy

12

<210> 39  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:degenerate  
probe for consensus gamma-conopeptide sequence.

<400> 39  
sartgytgyt cn

12

<210> 40  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
pro-gamma-conopeptide sequence for probe.

<400> 40  
Ile Leu Leu Val Ala Ala Val Leu  
1 5

<210> 41

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:degenerate  
 probe for consensus pro-gamma-conopeptide  
 sequence.

<400> 41  
 athythyng tngcngcngt nytn

24

<210> 42  
 <211> 32  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residues 14 and 26 are  
 gamma-carboxyglutamate; Xaa at residue 31 is  
 hdroxy-Pro.

<400> 42  
 Asp Cys Thr Ser Trp Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys  
 1 5 10 15  
 Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser  
 20 25 30

<210> 43  
 <211> 27  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residues 9 and 13 are  
 gamma-carboxyglutamate.

<400> 43  
 Cys Gly Gly Tyr Ser Thr Tyr Cys Xaa Val Asp Ser Xaa Cys Cys Ser  
 1 5 10 15

Asp Asn Cys Val Arg Ser Tyr Cys Thr Leu Phe  
 20 25

<210> 44  
 <211> 8  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> MOD\_RES  
 <222> (2)  
 <223> Xaa at residue 2 is carboxymethylCys

<400> 44  
Asp Xaa Thr Ser Trp Phe Gly Arg  
1 5

<210> 45  
<211> 24  
<212> PRT  
<213> Conus pennaceus

<220>  
<221> PEPTIDE  
<222> (1)..(24)  
<223> Xaa at residues 6 and 18 are  
gamma-carboxyglutamate; Xaa at residue 23 is  
hydroxy-Pro.

<400> 45  
Xaa Thr Val Asn Ser Xaa Xaa Xaa Ser Asn Ser Xaa Asp Gln Thr Tyr  
1 5 10 15  
Xaa Xaa Leu Tyr Ala Phe Xaa Ser  
20

<210> 46  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for M13  
universal priming site.

<400> 46  
tttcccagtc acgacgtt

18

<210> 47  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for M13  
reverse priming site.

<400> 47  
cacacaggaa acagctatg

19